

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 11, 2002, 12:13:28 ; Search time 39.17 Seconds
(without alignments)
2852.699 Million cell updates/sec

Title: US-09-841-132-190
Perfect score: 5238
Sequence: 1 MASMTGGQGMGRDSSLVPHH.....YFYRDASRGYGLSAGSKVRF 1006

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5238	100.0	1006	22	Protein encoded by
2	5231	99.9	1006	21	C. trachomatis pmp
3	5094	97.3	982	21	C. trachomatis pmp
4	5094	97.3	982	22	Protein encoded by
5	5090	97.2	1012	20	C. trachomatis LGV

ALIGNMENTS

AAG83207
ID AAG83207 standard; Protein; 1006 AA.
XX
AC AAG83207;
XX
DT 05-SEP-2001 (first entry)
XX
DE Protein encoded by Chlamydia trachomatis pmpG gene.
XX
KW Chlamydia; vaccine; infection; fusion protein; antigen;
KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
KW acute respiratory tract infection; Capi; CT529; OMCB;
KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
XX
OS Chlamydia trachomatis.
XX
PN WO20010474-A2.
XX
PD 07-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32919.
XX
PR 03-DEC-1999; 99US-0454584.
PR 19-APR-2000; 2000US-0556877.
PR 20-JUN-2000; 2000US-0598419.
XX
PA (CORI-) CORIXA CORP.
XX
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
XX
XX WPI; 2001-374831/39.
XX
PT Chlamydia polypeptides and fusion proteins useful for preventing pelvic
PT inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease
XX
PS Claim 2; Page 214-216; 295pp; English.
XX
CC The present sequence is provided in a specification relating to
CC compounds and methods for the treatment and diagnosis of chlamydial
CC infection. The compounds provided include polypeptides and fusion
CC proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX
SQ Sequence 1006 AA:

Query Match 100.0%; Score 5238; DB 22; Length 1006;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASMTGGQGMGRDSSLVPHHHHMFQGIYDGETLVSPFYTIVGDPSCGTFVSAGELT 60
Db 1 masmtggqgmgrdsslvpghhhhmipggydgetlvtvsfpytvgdpsgtvfsagelt 60

Qy 61 LKNLDNSIAALPLSCFCNLLGSFTVLGRGSLTFENIRSTNGAALNSAADGLFTIEGF 120
Db 61 lknldnsiaalpiscfnllgsftvlgrghsltfenirtstngaalnsaadglftiegf 120

Qy 121 KELSFSNCNSLLAVLPAATNKGSTPTTSTPSNGITYSKTDLNNEKFSFYNLVS 180
Db 121 kelsfscnslavlpaaatnkgstpttstpsngitysktdllnnekfsfynlvs 180

Qy 181 GDGGAIDAKSLTVQGISKLCVFQENTAQADGACQVVTFSAMANEAPIAFVANVAGVRG 240
Db 181 gdggaidaksltvqgisklcvfqentagdgacqvvtfsamaneapiafvanvagr 240

Qy 241 GGIAAAGVGGQGVSSSTSTEDPVVFSFRNTAVFEDGNVARVGGGIYSYGNVAFLNNGKTL 300
Db 241 ggiaaavdgqgvssststedpvsfrntavfdgnvarvvggiysygnvaflnngk 300

QY 301 FLNNVAPVYIAAKOPTSGOASNTSNNGDGAIFCKNGAQAGSNSSVSFDEGEGVVF 360
 Db 301 flnnvaspvyiaakoptsgoasntsnnyggdgaifckngagaqsgnssvsfdgegvvff 360
 QY 361 SSNVAAGKGGAIYAKKLSVANCVPVQLRNANDGGAIYLGESGELSADYGDIIFDGN 420
 Db 361 ssnvaagkggaiyakklsvancvpqvlrniandggaiylgesgelsadygdilfdgn 420
 QY 421 LKRTAKENAADVNGVTSSQAISMGSGKITTLLRAKAGHQILFNDPIEMANGNNQPAOSS 480
 Db 421 lkrtakenaadvngvtssqaismgsgkittllrakaghqilfndpiemangnnqpqass 480
 QY 481 KLLKINDGEGYTDIVFANGSSTLYQNVTTQGRIVLRERAKLSVNSISQTSGLYWEAG 540
 Db 481 kllkindgegytdivfangsstlyqnvttqgrivlreraklsvnsisqtgsglyweag 540
 QY 541 STLDFTVTPPPQPPAAANQLITLSLHLSLSSLLANNAVTPNPPAQBDSHPAVIGSTT 600
 Db 541 stldftvtpppqpqaanqlitlsnlhslslsllannavtnpnpqbdsphpavigstt 600
 QY 601 AGSVTISGPIFFEDLDATVDRYDWLGSNQKINVLKQLGKTPPANAPSDLTIGNEMPKY 660
 Db 601 agsvtisgpiiffedldatvdrdydwlgsgnkinkvlqglgktppanapsdltignemky 660
 QY 661 GYQGSWLAMPDNTANNPVTLLKATWTKGYNPGPERVASLVPNSLWGSILDIRSAHAI 720
 Db 661 gyqgsowlampdntannpvtllkatwtkgyngpgervaslvpnslwgsildirshai 720
 QY 721 QASVDGRSYRCGLWVSGVSNFFYHDDRDLGQGYRIISGGYSLGANSYFGSSMFLAFTEV 780
 Db 721 qasvdgrsyrcglwvsgvsnffyhddrdalggyryiisggyslgansyfgssmflaftev 780
 QY 781 FGRSKDYVVCBSNHHACIGSVYLSLQALCGSYLFGDAFTRASYGFGNQHMKTSYTFAE 840
 Db 781 fgrskdyvvcbsnhhacigsvylslqalcg sylfgdaftrasygfgnqhmktsytfae 840
 QY 841 SDVRWNNCLAGETGAGLPVITPESKLYLNLPRFVQAEFSYADHESFTEEGDQARAFKS 900
 Db 841 sdvrwnncclagetgaglpv itp es klylnlprf vqae f syadhes f teegdqarafks 900
 QY 901 GHLNLNVPGVKFDRCSSTHPNKYSFMAAYICDAYRTISGETFTLLSHOETWTTDAFHL 960
 Db 901 ghlnlnvpgv k fdr cs sthpnkysfmaayicdayrtisgetftllshoetwttdafhl 960
 QY 961 ARHGVVVRGSMYASLTSNIEVYGHGRYEYRDASRGYGLSAGSKVRF 1006
 Db 961 arhgvvvrgsmyas ltsnievyghgr yeyrda sr gygl sag skvrf 1006

RESULT 2

AAB13639
 ID AAB13639 standard; Protein: 1006 AA.

XX AC AAB13639;

XX DT 02-FEB-2001 (first entry)

XX DE C. trachomatis pmpG gene protein.

XX KW Chlamydial infection; sexually transmitted disease;
 KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
 KW trachoma; blindness; acute respiratory tract infection;
 KW atherosclerosis; coronary heart disease; antibacterial.

XX OS Chlamydia trachomatis.

XX PN WO200034483-A2.

XX PD 15-JUN-2000.

XX PF 08-DEC-1999; 99WO-US29012.

XX

PR 08-DEC-1998; 98US-0208277.
 PR 08-APR-1999; 99US-0288594.
 PR 01-OCT-1999; 99US-0410568.
 PR 22-OCT-1999; 99US-0426571.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
 XX
 XX WPI: 2000-431303/37.
 XX
 PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
 PT comprises immunogenic portion of Chlamydia antigen, which comprises
 PT amino acid sequence encoded by polynucleotide sequence
 XX
 PS Claim 2: Pages 208-210; 256pp; English.
 XX
 CC The present invention relates to new nucleic acid sequences and the
 CC proteins encoded by the nucleic acid sequences. The encoded proteins
 CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
 CC proteins are useful for the serodiagnosis and treatment of Chlamydia
 CC infection. Chlamydiae are intracellular bacterial pathogens that are
 CC responsible for a wide variety of human infections. C. trachomatis
 CC infection is one of the most common sexually transmitted diseases and can
 CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
 CC and infertility. Trachoma due to ocular infection with C. trachomatis is
 CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
 CC major cause of acute respiratory tract infections in humans and is also
 CC thought to play a role in the pathogenesis of atherosclerosis and
 CC coronary heart disease. The present sequence is a protein isolated in the
 CC present invention.
 XX
 SQ Sequence 1006 AA;
 Query Match 99.9%; Score 5231; DB 21; Length 1006;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1005; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MASMTGGQQGRSSLLVPHHHHHMIPQGIYDGETLTVSPYVIGDPSTTVFSAGELT 60
 Db 1 masmtggqgrdsslvphhhhhmipqgiydgeltvtvspyvigtsttvtfsagelt 60
 QY 61 LKLNDSIAALPLSCFNLGSLFTVLCGRGHSILTFENIRTSNGAALSAAADGLFTIEGF 120
 Db 61 lkln dsiaalplscfngslftvlg rghsltfenir tsn gaalsaaadglftiegf 120
 QY 121 KELSFSNCNSLLAVLPAATTNKGSTPTTTTSPSNGTIYSKTDLLLNNEKFSFYSNLVS 180
 Db 121 kelsfscn cnsllavlpaa ttnkgsqtpttstpsngtiysktdlllnnekfsfynlvs 180
 QY 181 GDGATDAKSLTVQGTISKLCVFOENTAAQDGGACQVTSFSAMANEAPIAFVANVAVRG 240
 Db 181 gdga tda ksltvqgtisklc vfoentaa qdg gacqvtsf samaneapiafvanvavrg 240
 QY 241 GGIAAVQDGGQGVSSSTSTEDPVVFSRNTAVEFDGNVARVGGIYSGYGNVAFLLNGKTL 300
 Db 241 ggiaav qdggqgvssststedpvv fsrntavefdgn varv ggiysgygnvafllngktl 300
 QY 301 FLNNVAPVYIAAKOPTSGOASNTSNNGDGAIFCKNGAQAGSNSSVSFDEGEGVVF 360
 Db 301 flnnvaspvyiaakoptsgoasntsnnyggdgaifckngagaqsgnssvsfdgegvvff 360
 QY 361 SSNVAAGKGGAIYAKKLSVANCVPVQLRNANDGGAIYLGESGELSADYGDIIFDGN 420
 Db 361 ssnvaagkggaiyakklsvancvpqvlrniandggaiylgesgelsadygdilfdgn 420
 QY 421 LKRTAKENAADVNGVTSSQAISMGSGKITTLLRAKAGHQILFNDPIEMANGNNQPAOSS 480
 Db 421 lkrtakenaadvngvtssqaismgsgkittllrakaghqilfndpiemangnnqpqass 480
 QY 481 KLLKINDGEGYTDIVFANGSSTLYQNVTTQGRIVLRERAKLSVNSISQTSGLYWEAG 540
 Db 481 kllkindgegytdivfangsstlyqnvttqgrivlreraklsvnsisqtgsglyweag 540

Db 481 kllkindgeygtdivfangsstlyqnvitieggrivlrekaklsvnslsqtgsglymeag 540
 QY 541 STLDFVTPQPPQPPAANLITLSNLHLSSLLANNVTPNPPAODSHPAVIGSTT 600
 Db 541 stldfvtppqpqpaaanqlitlsnlhlssllannavcnpptnppaqdshpavigstt 600
 QY 601 AGSVTISGPFFEDLDTPAYDRYDLGWSNQKINVLKQLGCTKPPANAPSDLTLCNEMPKY 660
 Db 601 agsvtisgpiffedldtadydrydwlsgngklnvklqlgctkppanapsdltlgnempsy 660
 QY 661 GYQGSWKLANDPNTANNPPTLKATWTGTYGNGPPEPVSILVPSNLWGLSILDIRSAHSAI 720
 Db 661 gyqgswklawdpntannpptylkatwtktgtyngpnpervasilvpsnlwgsildirsaasai 720
 QY 721 QASVDGSRGCLWVSGVSNFFYHDDRDLGOGYRISGGYSLGANSYFGSGSMFGLAFTEV 780
 Db 721 qasvdgsrcglwvsgvsnffyhddrdalgggyryisggyislgansyfgsgsmfglaftev 780
 QY 781 FGRSKDYVCRSNHHACIGSVYISTQOALCGSYLFGDAFIRASYGNGHMKTSYTFAAE 840
 Db 781 fgrskdyvcrsnhhacigsvylstqalcgsvylfgdafirasgygngqhmktstytfaee 840
 QY 841 SDYRWDNCLAGEIGAGLPVIPSCKLYLNLPRFVQAEFSYADHESFTTEGDAQAFKS 900
 Db 841 sdvrwdnclageigaglpvipscklylnelprfvqaefsyadhesfteegdqarafs 900
 QY 901 GHLLNLSPVPVGVKFDRCSTHPNKSYPMAAYICDAYRTISGTETTLTSHOETWTDAFHL 960
 Db 901 ghllnlsvpvgvkvfdrcssthpnkysfmaayicdayrtisgtetltlshoetwtldafhl 960
 QY 961 ARHGCVVGRGSMYASLTNIEVYGHGREYRDASKGYGLSAGSKVRF 1006
 Db 961 arhgcvvgrgsmyasltnievyghgreyrdasrgyglsgskvrf 1006

RESULT 3
 AAB13633
 ID AAB13633 standard; Protein: 982 AA.
 XX AC AAB13633;
 XX DT 02-FEB-2001 (first entry)
 XX DE C. trachomatis pmpG gene protein.
 XX KW Chlamydial infection; sexually transmitted disease;
 KW pelvic inflammatory disease; PID; tubal obstruction; infertility;
 KW trachoma; blindness; acute respiratory tract infection;
 KW atherosclerosis; coronary heart disease; antibacterial.
 XX OS Chlamydia trachomatis.
 XX PH Key Location/Qualifiers
 FT Misc-difference 981 /note= "Unspecified amino acid"
 FT WC2000034483-A2.
 XX PN 15-JUN-2000.
 XX PD 08-DEC-1999; 99WO-US29012.
 XX PF 08-DEC-1998; 98US-0208277.
 XX PR 08-APR-1999; 99US-0288594.
 XX PR 01-OCT-1999; 99US-0410568.
 XX PR 22-OCT-1999; 99US-0426571.
 XX PA (CORI-) CORIXA CORP.
 XX PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
 XX WPI; 2000-431303/37.
 XX

PT Isolated polypeptide for diagnosis and treatment of Chlamydia infection
 PT comprises immunogenic portion of Chlamydia antigen, which comprises
 PT amino acid sequence encoded by polynucleotide sequence -
 XX Claim 2; Pages 181-184; 256pp; English.
 XX The present invention relates to new nucleic acid sequences and the
 CC proteins encoded by the nucleic acid sequences. The encoded proteins
 CC comprise an immunogenic portion of a Chlamydia antigen. The encoded
 CC proteins are useful for the serodiagnosis and treatment of Chlamydia
 CC infection. Chlamydiae are intracellular bacterial pathogens that are
 CC responsible for a wide variety of human infections. C. trachomatis
 CC infection is one of the most common sexually transmitted diseases and can
 CC lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
 CC and infertility. Trachoma due to ocular infection with C. trachomatis is
 CC the leading cause of preventable blindness worldwide. C. pneumoniae is a
 CC major cause of acute respiratory tract infections in humans and is also
 CC thought to play a role in the pathogenesis of atherosclerosis and
 CC coronary heart disease. The present sequence is a protein isolated in the
 CC present invention.
 XX Sequence 982 AA;
 SQ

Query Match 97.3%; Score 5094; DB 21; Length 982;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 981; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 25 MIQGIYDGETLVSPFYTIVIGDPSGTTVFSAGELTLKLDNSTAALPLSCFGLNLSFT 84
 Db 1 mipqgiydgeltvsvfytivigdpstgtvifsageltlknldnsaalplscfgnllgsft 60
 QY 85 VLGRGHSLTENIRTSNNGAALNSAADGLFTIEGKELSFSCNLSLAVLPAAATTKGS 144
 Db 61 vlgrghsltenirtstngaalsnsaadglftiegkelsfscnslavlpaaattnkgs 120
 QY 145 QTPTTSTPSNGTIYKTDLLLNNKEFSYSLNLSVSDGGAIDAKSLTVGICSLCVFQE 204
 Db 121 qtpttstpsngtiysktdlllnnekfsynlsvsdggaidaksltvvgisklvfqe 180
 QY 205 NTAQADGGACQVTVFSAMANEAPIAVNAVVRGGIAAVQDGGQGVSSSTSTEDPVV 264
 Db 181 ntaqadggacqvvtfsamaneapiaevnavvrggiaavqdgqgvssststedpvtv 240
 QY 265 SFSRNTAVEFDGNVARGGGIYSGNVAFNLNNGKTLFLNNVASPVYIAAKOPTSGQASNT 324
 Db 241 sfsrntavefdgnvarvggiysgnavflnngktlflnnvaspvyaakoptsgqasnt 300
 QY 325 SNNYGDDGGAIFCKNGAQAQSNNSGVSFDDGGVGVFFSSNVAAGKGAIYAKKLSVANCGP 384
 Db 301 snnygddggaifckngaqaqsnnsqsvsfddggvvgvffssnvaagkgaiyakklsvancgp 360
 QY 385 VQFLRNTANDGGAIYLGESGELSADYGDIIIFDGNLKRKAKENAAADVNGTVSSQAISM 444
 Db 361 vqflrntandggaiylgesgelsadygdiiifdgnlkrakenaadvngvtvssqaism 420
 QY 445 GSGGKITTLRAKAGHQILFNDPIEMANGNNQPAQSSKLLKINDGEGYTGDIIVFANGSSTL 504
 Db 421 gsggkittlrakaghqilfndpiemangnnqpqsskllkindgegytgdivfangsstl 480
 QY 505 YQNVTFEGRIVLREKAKLSVNSLSQTGSLYMEAGSTLDFVTQPQPQPPAANQLITLS 564
 Db 481 yqnvtfeggrivlrekaklsvnslsqtgsglymeagstldfvtqpqpqpaaanqlitls 540
 QY 565 NLHLSSLILLANNAVTPNPPAODSHPAVIGSTTISGPIFFEDLDTPAYDRYD 624
 Db 541 nlhlsslillannavtpnppaqdshpavigsttisgpiiffedldtdaydryd 600
 QY 625 WLGSNOKINVLKQLGCTKPPANAPSDLTLCNEMPKYQGSWKLAWDPNTANNPPTLKA 684
 Db 601 wlgsnokinvlkqlgctkppanapsdltlcnempkyqgswklawdpntannpptylka 660
 QY 685 TWTKTGYNPGERVASLVPNSLWGLSILDIRSAHSAIQASVDGSRGCLWVSGVSNFFYH 744

|||||
Db 661 twtkgynpervvaslvpsnlwsglildirsahsaicqsdvgrscrglwgsvgsnffyh 720
QY 745 DRDALGQYRIISGGYISLGANSYFGSSMFLAFTTEVFGRSKDYVVCRSNHACIGSYLS 804
Db 721 drdalgggyryisggyslgansyfgsmfglaftevfgrskdyvvcrsnhhacigsvls 780
QY 805 TQOALCGSYLFGDAFIRASYGFGNOHMKTSYTFAEESDVRDNNCLAGETCAGLPVITP 864
Db 781 tqqalcgsyifgdafirasylfngqhmktstytfaeesdvrwnncilageigaglpvitp 840
QY 865 SKLYNELRPFVQAEFYADHESFTTEGDOARAFKSGHLLNLSVPVGVKFDRCSSSTHPNK 924
Db 841 sklynelrpfvqaeфыadhesfteegdqarafksgghllnlsvpvgvkfdrcssthpnk 900
QY 925 YSFMAAICDAYRTISGTETLLSHQETWTDAPHLARHGWWVRGSMYASLTSNIEVYGH 984
Db 901 ysfmaayicdayrtisgtetllshqetwttdafhlarhgvvvrsgmsyasltsnievygh 960
QY 985 GRYEYRDASRGYLSAGSKVRF 1006
Db 961 gryeyrdasrgyylsagskvxf 982

RESULT 4
AAG83201
ID AAG83201 standard; Protein; 982 AA.
XX
AC AAG83201;
XX
DT 05-SEP-2001 (first entry)
XX
DE Protein encoded by Chlamydia trachomatis pmpG gene.
XX
KW Chlamydia; vaccine; infection; fusion protein; antigen;
KW pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
KW acute respiratory tract infection; CapI; CT529; OMCB;
KW polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
XX
OS Chlamydia trachomatis.
XX
PN W0200140474-A2.
XX
PD 07-JUN-2001.
XX
PE 04-DEC-2000; 2000WO-US32919.
XX
PR 03-DEC-1999; 9905-0454684.
PR 19-APR-2000; 2000US-0556877.
PR 20-JUN-2000; 2000US-0598419.
XX
XX (CORI-) CORIXA CORP.
PA
PI Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
XX
XX WPI; 2001-374831/39.
XX
XX Chlamydia polypeptides and fusion proteins useful for preventing pelvic
PT inflammatory disease, trachoma, acute respiratory tract infections,
PT atherosclerosis and heart disease -
XX
XX Claim 2; Page 189-191; 295pp; English.
XX
XX The present sequence is provided in a specification relating to
CC compounds and methods for the treatment and diagnosis of chlamydial
CC infection. The compounds provided include polypeptides and fusion
CC proteins comprising immunogenic portions of Chlamydia antigens
CC and DNA sequences encoding such polypeptides. They are useful for
CC vaccinating against chlamydial infection, which causes pelvic
CC inflammatory disease, trachoma, acute respiratory tract infections,
CC atherosclerosis and heart disease.
XX
SQ Sequence 982 AA;

Query Match 97.3%; Score 5094; DB 22; Length 982;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 981; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 25 MIPQGIYDGETLVSPFYTIVIGDPSTGTTVFAGELTLKLNLDNSTAAALPLSCFNGLLCSFT 84
Db 1 mipqgiydgeltvsvfytvigrpsgtctvfageltklndnsiaalpplscfngllgsft 60
QY 85 VLGRGHSLTFFENIRTSNTGAALSNSAADGLFTIEGKELSFNSNCNSLLAVLPAATTNKG 144
Db 61 vlgrghsiltfenirtstngaalsnsaadgltiegfkelsfnsncnsllavlpaattnkgs 120
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Db 121 qtpttstspngtiysktdllllnnekfstynlvsgdgaidaksltvgigsklcvfqe 180
QY 205 NTAQADGGACQVVTFSAMANEAPIAFVANVAVRGGGIAAVDGGQGVSSSTSTEDPVV 264
Db 181 ntaqadggacqvvtfsamaneapiafvanvavrgggiaavdgqgvssststedpvv 240
QY 265 SFSRNTAVEFDGNVARVGGGIYSYGNVAFLLNGKTLFLNNVASPVYIAAKOPTSGQASNT 324
Db 241 sfsrntavefdgnvarvgggiysygnvafllngktlflnnvaspvylaaakoptsgaesnt 300
QY 325 SNYGGCGAIFCKNGAAGSNNSGSVSFDGEGVVFSSNVAAGKGGAIYAKKLSVANC 384
Db 301 snnyggcgai fckngaagsnnsgsvsfdgegvvffssnvaagkggaiyakklsvancgp 360
QY 385 VQFLRNANDGGAIYLGESGELSLSADYDGIIPDGNLKRRTAKENAADVNGVTVSSQAISM 444
Db 361 vqflrniandggaiylgesgelslsadydgiiidgnlkrktakenaadvngvtvssqaism 420
QY 445 GSGGKITTLRAKQHQLFNDPIEMANGNNQPAQSSKLLKINDGEGYTGDIVFANGSSTL 504
Db 421 gsggkittlrakaghqilfndpiemangnnqpqgsskllkindgegytgdivfangsstl 480
QY 505 QONVTIEGGRIVLREKAKLSVNSLSQTGGSLYMEAGSTLDFVTPQPPQPPAANQLITLS 564
Db 481 yonvtiegrivlrekaklsvnslsqtggslymeagstldfvtpqppqppaanelitls 540
QY 565 NLHLSLSLLANNNAVTPNPAPQDSHPAVIGSTTAGSVTISQIPIFFELDDTAYDRYD 624
Db 541 nlhlsllsllannnavtpnpnpqdsphavigsttagsvtisgpiiffelddtaydryd 600
QY 625 WLGSNOKINVLKLOLQTKPPANAPSDTLGNEMPKYGYQGSWKLWDPNTANNNGPYTLKA 684
Db 601 wlgsnokinvlkqlgtkppanapsdltlgnempkygyqgswklawdpntannngpytlka 660
QY 685 TWTKTGYNPGPERVASIAPNSLMGSLTDIRSAHSAIOASVDGRSYCRLWVGVSNEFFYH 744
Db 661 twtktgynpgpervvasilvpsnlwsglildirsahsaicqsdvgrscrglwgsvgsnffyh 720
QY 745 DRDALGQYRIISGGYISLGANSYFGSSMFLAFTTEVFGRSKDYVVCRSNHACIGSYLS 804
Db 721 drdalgggyryisggyslgansyfgsmfglaftevfgrskdyvvcrsnhhacigsvls 780
QY 805 TQOALCGSYLFGDAFIRASYGFGNOHMKTSYTFAEESDVRDNNCLAGETCAGLPVITP 864
Db 781 tqqalcgsyifgdafirasylfngqhmktstytfaeesdvrwnncilageigaglpvitp 840
QY 865 SKLYNELRPFVQAEFYADHESFTTEGDOARAFKSGHLLNLSVPVGVKFDRCSSSTHPNK 924
Db 841 sklynelrpfvqaeфыadhesfteegdqarafksgghllnlsvpvgvkfdrcssthpnk 900
QY 925 YSFMAAICDAYRTISGTETLLSHQETWTDAPHLARHGWWVRGSMYASLTSNIEVYGH 984
Db 901 ysfmaayicdayrtisgtetllshqetwttdafhlarhgvvvrsgmsyasltsnievygh 960
QY 985 GRYEYRDASRGYLSAGSKVRF 1006
Db 961 gryeyrdasrgyylsagskvxf 982

RESULT 5
 AAY16735
 ID AAY16735 standard; Protein; 1012 AA.
 AC AAY16735;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE C. trachomatis LGV L2 HMW protein.
 XX
 KW Chlamydia; high molecular weight protein; HMW protein; urethritis;
 KW bacterial infection; conjunctivitis; lymphogranuloma venereum; LGV;
 KW cervicitis; epididymitis; endometritis; pelvic inflammatory disease;
 KW PID; salpingitis; tubal occlusion; infertility; cervical cancer;
 KW arteriosclerosis; atherosclerosis.
 XX
 OS Chlamydia trachomatis.
 XX
 PN WO9917741-A1.
 XX
 PD 15-APR-1999.
 XX
 PF 01-OCT-1998; 98WO-US20737.
 XX
 PR 02-OCT-1997; 97US-0942596.
 XX
 PA (ANTE-) ANTEX BIOLOGICS INC.
 XX
 PI Jackson JW, Pace JL;
 XX
 DR WPI: 1999-287659/24.
 DR N-PSDB; AAX60539.
 XX
 PT New Chlamydia protein useful for treating conjunctivitis, urethritis
 PT and cervical cancer
 XX
 PS Claim 4; Fig 3; 141pp; English.
 XX
 CC The invention relates to an isolated Chlamydia species high molecular
 CC weight (HMW) protein having an apparent mol. wt. of 105-115 kD as
 CC determined by SDS-PAGE. The HMW proteins and nucleic acid molecules can
 CC be used for preventing, treating or ameliorating a disorder related to
 CC Chlamydia e.g. bacterial infection, conjunctivitis, urethritis,
 CC lymphogranuloma venereum (LGV), cervicitis, epididymitis, endometritis,
 CC pelvic inflammatory disease (PID), salpingitis, tubal occlusion, cervical
 CC cancer, infertility, arteriosclerosis and atherosclerosis. The products
 CC can also be used for detection and diagnosis. The present sequence
 CC represents a C. trachomatis HMW protein.
 XX
 SQ Sequence 1012 AA;

Query Match 97.2%; Score 5090; DB 20; Length 1012;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 979; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 MIPQGIYDGETLVSPFTVIGDPSGTVFSGAGELTKNLNDSIAALPLSCFNLGSGFT 84
 Db 31 mvpqgiydgeltvspftvigtvsgageltknlndnsiaalpiscfnglsgft 90
 QY 85 VLGRGHSITFENIRSTNGAALSNSAAGLFTIEGFKELSFNSCNLLAVLPAATTNKG 144
 Db 91 vlgrghsltfenirstngalsnsaaglfteiegkelsfnsncnllavipaattnkg 150
 QY 145 QTPPTTSPNGTIYSKTDLLLNNEKFSFYSLNLSVGDGGAIDAKSLTVQGISKLCVFEQ 204
 Db 151 qtpttstpsngtiysktdlllnneksfylnsvsgdgaidskltvqgisklcvfeq 210
 QY 205 NTAQADGACQVVTFSFMANEAPITAFVANVAGVRGGIAAVQDQCGQVSSSTSTEDPV 264
 Db 211 ntaqadgacqvvtfsfmaneapitafvanvavrgggiaavqdqgqvgvssststpdvv 270.

QY 265 SFSRNTAVEFDGNVARVGGIYSYGNVAFNLNNGKTLFLNNVASPVYIAAKOPTSGOASNT 324
 Db 271 sfsrntavefdgnvarvvggiysygnvafnlngkklflnnvaspvyaakqptsqasnt 330
 QY 325 SNNYGDGGAIFCKNGAQAGSNNSGSVSPDGEVWFSSNVAAGKGAIIYAKKLSVANGCP 384
 Db 331 snnygdggaifckngaqagsnnsgrsvfdgevvffssnvaagkggaiysvancgp 390
 QY 385 VOFLRNANDGGAIIYLGESGELSADYGDIIIFDGNLRTAKENAADVNGVTVSSQAISM 444
 Db 391 vqflrniandggaailylgesgelsadygdliifdgnlkrtakenaadvngvtvssqaism 450
 QY 445 GSGGKITTLRAKAGHOILFNDPIEMANGNNOQAOSKLLKINDGSGYTGDIIVFANGSSYFL 504
 Db 451 gsggkittlrakaghqilfndpiemangnnpagaskllkndgegytgdvifangsstl 510
 QY 505 YONVTIEQGRIVLREKAKLSVNSLSQTGGSLYMEAGSTLDFVTPPOPPAANOLITLS 564
 Db 511 yqnvtieqgrivlrekaklsvnsisqtggslymeagstwdfvtpppgqppaanglitis 570
 QY 565 NLHLSLSLLANNVNTNPPTPAQDSHPAVIGSTTAGSVTISGPIFFEDLDDTAYDRYD 624
 Db 571 nlhlsllsllannavntnpptpaqdsbpavigsttagsvtisgpiiffedlddtaydryd 630
 QY 625 WLGSNOKINVLKQLGTPKANAPSDLTLGNEMPKYGYQGSWKLAWDPNTANNPVTLKA 684
 Db 631 wlgsnokinvlkqlgtkpanapdsdltnemphygyqgswklawdpntannpvtlka 690
 QY 685 TWTKTGYNPGPERVASLVPNSLWMSILDIRSAHSIAQASVDGSRGYCRGLWVSGVSNFFVH 744
 Db 691 twtktyngpgpervaslvpnslwmsildirsaahsaigasvdgrsgyrcrglwvsgvsnffv 750
 QY 745 DRDALGCGYRYISGGYSLGANSYFGSSMFGLAFTVFGSRKDYVVCRSNHHACIGSVYLS 804
 Db 751 drdalgggyryisggyslgansyfgssmfglaftevfgrskdyvvcrrsnhhacigsvyls 810
 QY 805 TQOALCGSYLFGDAFIRASYFGNOHMKTSYTFABESDVRMDNCLAGEIGAGLPVITP 864
 Db 811 tqqalcgysylfgdafirasyfgnqhmktstfbaesdvrdnncclageigaglpvityp 870
 QY 865 SKLYLNEURPVQAEFSYADHESFTEEGDQARAFKSGHLLNLSPVGVKFDRCSTHPNK 924
 Db 871 sklylneirpvtqaeysyadhesfteegdqarafkshllnlsvpgvkvfdrcssthpkn 930
 QY 925 YSFMAAYICDAYRTISGTETTLTSHOETWTTDAFHLAGHVGVVGRGSMVASLTNSIEVYGH 984
 Db 931 ysfmaayicdayrtisgtettllshqetwttdafhlaghvvgvrgsmvasltsnievygh 990
 QY 985 GRYEYRDASRGYGLSAGSKVRF 1006
 Db 991 gryeyrdasrgyglisagrvrf 1012

Search completed: September 11, 2002, 12:32:05
 Job time: 1117 sec

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OM protein - protein search, using sw model

Run on: September 11, 2002, 12:28:33 ; Search time 25.91 seconds
(without alignments)
3730.832 Million cell updates/sec

Title: US-09-841-132-190

Sequence: 5238
1 MASMTGGQGMGRDSSLVPHH.....YKRDASRGYGLSAGSKVRF 1006

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 45 summaries

Database: PIR-71
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4986.5	95.2	1013	2	G71460 Probable outer mem

ALIGNMENTS

RESULT 1
G71460
Probable outer membrane protein G - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: G71460
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; M0ID:99000809
A:Accession: G71460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1013 <ARN>
A:Cross-references: GB:AE001360; GB:AE001273; NID:g3329342; PIDN:ANC6469.1; PID:g332934
A:Experimental source: Serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: pmpG

Query Match 95.2%; Score 4986.5; DB 2; Length 1013;
Best Local Similarity 97.4%; Pred. No. 2.3e-294;
Matches 957; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

QY	25	MIPOGIYDGETLTVSPFYTVIGDPSGTTVESAGELTTLKNDLNSIAALPLSGFNLGSGFT	84
DB	31	MIPOGIYDGETLTVSPFYTVIGDPSGTTVESAGELTTLKNDLNSIAALPLSGFNLGSGFT	90
QY	85	VLGRHSLTEFNITSTNGAALSAAADLFTIGFKELEFSNCSNLSLAVLPAATTNGKS	144
DB	91	VLGRHSLTEFNITSTNGAALSAAADLFTIGFKELEFSNCSNLSLAVLPAATTNGKS	150
QY	145	QTPTTSPNSNGTISTYSTDLLLNNEKFSFNSLVSDGGAIDAKSLTVGDISLVCPOE	204
DB	151	QTPTTSPNSNGTISTYSTDLLLNNEKFSFNSLVSDGGAIDAKSLTVGDISLVCPOE	210
QY	205	NTAADGACQCVYTSFSAMANEAPIAFVAVYAGRGGIAAODQOQGVSSSTEDPPVY	264
DB	211	NTAADGACQCVYTSFSAMANEAPIAFVAVYAGRGGIAAODQOQGVSSSTEDPPVY	270
QY	265	SFSRNTAVEEDGNVAVRGGIIYSYGNVAFPLNGKTLFLNNVAFVYIAAOPVSGQASNT	324
DB	271	SFSRNTAVEEDGNVAVRGGIIYSYGNVAFPLNGKTLFLNNVAFVYIAAOPVSGQASNT	330
QY	325	SNNYGDGGAIFCKNGAQ-AGSNNSGSVFQEGVFFSSNVAAGKGAIAAKLSVANCG	383
DB	331	SDNYGDGGAIFCKNGAQ-AGSNNSGSVFQEGVFFSSNVAAGKGAIAAKLSVANCG	390
QY	384	PVOFLRNINANDGAIYGESEGLSLADYGDIIFDGMLKRTAKENADVNGVTVSSQAS	443
DB	391	PVOFLRNINANDGAIYGESEGLSLADYGDIIFDGMLKRTAKENADVNGVTVSSQAS	450
QY	444	MGSGKITTLTRAKAGHOLFNDPIEMANGNNOPOASSKLKINDGEGYTDIYFANCSST	503
DB	451	MGSGKITTLTRAKAGHOLFNDPIEMANGNNOPOASSKLKINDGEGYTDIYFANCSST	510
QY	504	LYQWVTEEGRIYAREAKLSVNSLSTGGSLYWEASTLDFVTPPOPPQAPPAANOITL	563
DB	511	LYQWVTEEGRIYAREAKLSVNSLSTGGSLYWEASTLDFVTPPOPPQAPPAANOITL	570
QY	564	SNLHLSLSLANNAAVNPPTNPPODSHVAIGSTAGSVTSGPIFFEDLDPTAVADRY	623
DB	571	SNLHLSLSLANNAAVNPPTNPPODSHVAIGSTAGSVTSGPIFFEDLDPTAVADRY	630
QY	624	DWLGSNOKIVLKLQIGTKPPANASDLTIGENPKYGYGCSWKLAMPPTANNGPYTLK	683
DB	631	DWLGSNOKIVLKLQIGTKPPANASDLTIGENPKYGYGCSWKLAMPPTANNGPYTLK	690
QY	684	ATWTKTYGNPGRVAVASLVNSLMSGLDLSRAHSAIQASVDGRSRYGRLVSGVSNFFY	743
DB	691	ATWTKTYGNPGRVAVASLVNSLMSGLDLSRAHSAIQASVDGRSRYGRLVSGVSNFFY	750
QY	744	HDRDALGQGYRYTSGSYSLGANSYFGSSMGFLAFTEYFGRSKDYVVCRSNHHACIGSVYL	803
DB	751	HDRDALGQGYRYTSGSYSLGANSYFGSSMGFLAFTEYFGRSKDYVVCRSNHHACIGSVYL	810
QY	804	STOQALCGSYLFGDAFIRASVYFGNOMKTSYFAESDVARDNCLAGEIGALPIVIT	863
DB	811	STOQALCGSYLFGDAFIRASVYFGNOMKTSYFAESDVARDNCLAGEIGALPIVIT	870
QY	864	PSKLYLNELPFVQAESEYADHESFTEEGQAARFASGHLNLSVPYGVAFDRCSSTHPN	923
DB	871	PSKLYLNELPFVQAESEYADHESFTEEGQAARFASGHLNLSVPYGVAFDRCSSTHPN	930
QY	924	KYSFMAVYCDARTISGTTTLLSHOETWTTQAPFLHARGVAVRGSMAVSLNSIEVYG	983
DB	931	KYSFMAVYCDARTISGTTTLLSHOETWTTQAPFLHARGVAVRGSMAVSLNSIEVYG	990
QY	984	HGRYERDASRGYGLSAGSKVRF 1006	
DB	991	HGRYERDASRGYGLSAGSKVRF 1013	

Search completed: September 11, 2002, 12:32:59
Job time: 266 sec

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OM protein - protein search, using sw model

Run on: September 11, 2002, 12:32:28 ; Search time 15.1 seconds
(without alignments)
2579.594 Million cell updates/sec

Title: US-09-841-132-190
Perfect score: 5238
Sequence: 1 MASMTGGQGMGRDSSSLVPHH.....YEYRDSRGYGLSAGSKVRF 1006

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4986.5	95.2	1013	1 PMPG_CHLTR	084879 chlamydia t

ALIGNMENTS

RESULT 1		PMPG_CHLTR		STANDARD;		PRT; 1013 AA.	
ID	084879;	AC	084879;	DT	16-OCT-2001 (Rel. 40, Created)	DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last sequence update)	DT	16-OCT-2001 (Rel. 40, Last annotation update)	DE	Probable outer membrane protein pmpg precursor (Polymorphic membrane protein G).	DE	protein G).
GN	PMPG OR Ct871.	OS	Chlamydia trachomatis.	OC	Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.	OX	NCBI_TaxID=813;
RN	[1]	RP	SEQUENCE FROM N.A.	RC	STRAIN=D/UN-3/CX;	RX	MEDLINE=99000809; PubMed=9784136;
RA	Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;	RA	"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."	RL	Science 282:754-759(1998).	CC	-1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES) (POTENTIAL).
CC	-1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.	CC		CC		CC	

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).

DR EMBL: AE001360; AAC68469.1;
DR InterPro: IPR003368; DUF145.
DR InterPro: IPR003357; OMP.
DR Pfam: PF02415; DUF145; 1.
DR Pfam: PF02385; OMP; 1.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 1013 PROBABLE OUTER MEMBRANE PROTEIN PMPG.
SQ SEQUENCE 1013 AA; 107366 MW; F0927743C0A651DD CRC64;

Query Match 95.2%; Score 4986.5; DB 1; Length 1013;
Best Local Similarity 97.4%; Pred. No. 4.7e-286;
Matches 957; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

QY	25	MIPOGIYDGETLVSPFYTVIGDPSTVFSAGELTLKNDNSIAALPLSCFNLLGSFT	84
DB	31	MIPOGIYDGETLVSPFYTVIGDPSTVFSAGELTLKNDNSIAALPLSCFNLLGSFT	90
QY	85	VLGRGHSITFENIRTSNGAALSNSAAGLFTIEGKELSFSCNSLLAVLPAAITNKG	144
DB	91	VLGRGHSITFENIRTSNGAALSNSAAGLFTIEGKELSFSCNSLLAVLPAAITNNGS	150
QY	145	QTPTTSTPSNGIYKTKDLLLLLNNEKFSFYSLVSDGDAIDAKSLTVOGISKLCVQ	204
DB	151	QTPTTSTPSNGIYKTKDLLLLLNNEKFSFYSLVSDGDAIDAKSLTVOGISKLCVQ	210
QY	205	NTAQADGGACQVTSFSAMANEAPIAVNAVVGRIIAVVDGQGVSSSTSTEDPVV	264
DB	211	NTAQADGGACQVTSFSAMANEAPIAVNAVVGRIIAVVDGQGVSSSTSTEDPVV	270
QY	265	SFSRNTAVEFDGNVARGGGIYSGNVAFNNCKTLFLNNVAPVIAAKQPTSGOASNT	324
DB	271	SFSRNTAVEFDGNVARGGGIYSGNVAFNNCKTLFLNNVAPVIAAKQPTSGOASNT	330
QY	325	SNNYGDGAIFCKNGAQ-AGSNNSGVSFDGEGVFFSSNVAAGKGGIYAKKLSVANC	383
DB	331	SDNYGDGAIFCKNGAQAGSNNSGVSFDGEGVFFSSNVAAGKGGIYAKKLSVANC	390
QY	384	PVOFLNIANDGGAIYLGESGELSADYGDIIIDGNLKRKTAKENAAADVNGVTSSQA	443
DB	391	PVOFLNIANDGGAIYLGESGELSADYGDIIIDGNLKRKTAKENAAADVNGVTSSQA	450
QY	444	MGSGGKITTLRAKAGHOILFNDPIEMANGNNOQAQSSKLLKINDGEGYTGDI	503
DB	451	MGSGGKITTLRAKAGHOILFNDPIEMANGNNOQAQSSKLLKINDGEGYTGDI	510
QY	504	LYQNVTEQGRIVLREKAKLSVNSLSQTSGLSMEAGSTLDFVTPQPPQPPAANQITL	563
DB	511	LYQNVTEQGRIVLREKAKLSVNSLSQTSGLSMEAGSTLDFVTPQPPQPPAANQITL	570
QY	564	SNLHLSLLSLLANNVTPNPPNPAQDSHPAVIGSTTAGSVTISGPIFFEDLDDTAYDR	623
DB	571	SNLHLSLLSLLANNVTPNPPNPAQDSHPAVIGSTTAGSVTISGPIFFEDLDDTAYDR	630
QY	624	DWLGSNQKINVKLQJLQKTRPPANAPSDTLTGNEMPKYGYGSKWLAWDPNTANGPYTLK	683
DB	631	DWLGSNQKIDVLQJLQKTRPPANAPSDTLTGNEMPKYGYGSKWLAWDPNTANGPYTLK	690
QY	684	ATWTKGYNPGPERVASLPNSLWGSTLDIRSAHSAIQASVDGSRVCRGLWVGVSFFY	743
DB	691	ATWTKGYNPGPERVASLPNSLWGSTLDIRSAHSAIQASVDGSRVCRGLWVGVSFFY	750
QY	744	HDRDALGGQYRISGGYISLGANSYFGSSMFLAFTEVFGRSKDYVVCRRSHHACISVYL	803

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OM protein - protein search, using sw model

Run on: September 11, 2002, 12:32:08 ; Search time 40.86 Seconds
(without alignments)
4259.249 Million cell updates/sec

Title: US-09-841-132-190
Perfect score: 5238
Sequence: 1 MASMTGGQMGNDSSLVPHH.....YEYRDASRGYGLSAGSKVRF 1006

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
No matches found					

Search completed: September 11, 2002, 12:36:59
Job time: 291 sec

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OM protein - protein search, using sw model

Run on: September 11, 2002, 12:25:13 ; Search time 17.9 Seconds
(without alignments)
1372.746 Million cell updates/sec

Title: US-09-841-132-190
Perfect score: 5238
Sequence: 1 MASMTGGQQMGRDSSLVPHH.....YEVNDSRGYGLSAGSKVRF 1006

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
Description					

No matches found

Search completed: September 11, 2002, 12:32:25
Job time: 432 sec

